What is claimed is:

1. A process for determining whether or not a test sample originating from or containing human cells has a tumor progression potential, wherein a second sample originating from non-tumor cells from the same individual or a different individual of the same species is also used, which process comprises the following steps:

   (a) incubating said samples under stringent hybridization conditions with a nucleic acid probe which is selected from the group consisting of:
      (i) a nucleic acid with a sequence of SEQ ID NO:1 or a fragment thereof;
      (ii) a nucleic acid with a sequence which is complementary to any nucleic acid of (i);
      (iii) a nucleic acid with a sequence which hybridizes under stringent conditions with the nucleic acid of (i); and
      (iv) a nucleic acid with a sequence which hybridizes under stringent conditions with the nucleic acid of (ii); and
   (b) determining the approximate amount of hybridization of each respective sample with said probe and
   (c) comparing the approximate amount of hybridization of the test sample to an approximate amount of hybridization of said second sample to identify whether or not the test sample contains a lower amount of the nucleic acid than does said second sample.

2. A process for determining whether or not a test sample originating from or containing human cells has a tumor progression potential, which process comprises the following steps:

   (a) incubating a first compartment of said sample under stringent hybridization conditions with a first nucleic acid probe which is selected from the group consisting of:
      (i) a nucleic acid with a sequence of SEQ ID NO:1 or a fragment thereof;

(ii) a nucleic acid with a sequence which is complementary to any nucleic acid of (i);

(iii) a nucleic acid with a sequence which hybridizes under stringent conditions with the nucleic acid of (i); and

(iv) a nucleic acid with a sequence which hybridizes under stringent conditions with the nucleic acid of (ii); and

(b) incubating a second compartment of said sample under stringent hybridization conditions with a second nucleic acid probe being a housekeeping gene or a fragment thereof;

(c) determining the approximate amount of hybridization of said sample with said first and second probe;

(d) identifying whether or not the test sample contains an at least 3-fold amount of nucleic acid hybridizing with the first probe in comparison to the amount of nucleic acid hybridizing with the second probe.